```
feline (from cDNA)   YEIAPVFVLMEQITLKKMREIVGWSSKDGDGIFSPGGAISNMYSIMAARYKFFPEVKTKG
                     ------------->                                      <-------------
rat (from peptide)   YEIAPVFVLLEYV-----REIIGWPGGS-DGIFSPGGAISN-YAMLIARYKMFPEVKEKG
```

Figure 1

```
GGGCGTGCGGGGTCGAGCCGAAGCAGCTTGCCCGCAGCCACTCGGAGGCGACCAGCGCCA
       10                  30                  50
             M  A  S  P  G  S  G  F  W  S  F  G  S  E  D  G
GACTAGCAGAACCCATGGCATCTCCGGGCTCTGGCTTTTGGTCCTTCGGATCTGAAGATG
       70                  90                  110
  S  G  D  P  E  N  P  G  T  A  R  A  W  C  Q  V  A  Q  K  F
GCTCTGGGGATCCTGAGAACCCGGGAACAGCGAGAGCCTGGTGCCAGGTGGCCCAAAAGT
      130                 150                 170
  T  G  G  I  G  N  K  L  C  A  L  L  Y  G  D  S  E  K  P  A
TCACGGGCGGCATCGGAAACAAGCTATGCGCTCTGCTCTACGGAGACTCTGAGAAGCCAG
      190                 210                 230
  E  S  G  G  S  V  T  S  R  A  A  T  R  K  V  A  C  T  C  D
CAGAGAGCGGCGGGAGCGTGACCTCGCGGGCCGCCACTCGGAAGGTCGCCTGCACCTGTG
      250                 270                 290
  Q  K  P  C  S  C  P  K  G  D  V  N  Y  A  L  L  H  A  T  D
ACCAAAAACCCTGCAGCTGCCCCAAAGGAGATGTCAATTATGCACTTCTCCACGCAACAG
      310                 330                 350
  L  L  P  A  C  E  G  E  R  P  T  L  A  F  L  Q  D  V  M  N
ACCTGCTGCCAGCCTGTGAAGGAGAAAGGCCCACTCTCGCATTTCTGCAAGATGTAATGA
      370                 390                 410
  I  L  L  Q  Y  V  V  K  S  F  D  R  S  T  K  V  I  D  F  H
ACATTTTGCTTCAGTACGTGGTGAAAAGTTTTGATAGATCAACTAAAGTGATTGATTTCC
      430                 450                 470
  Y  P  N  E  L  L  Q  E  Y  N  W  E  L  A  D  Q  P  Q  N  L
ATTACCCCAATGAGCTTCTTCAAGAGTATAATTGGGAATTGGCAGACCAACCGCAAAATC
      490                 510                 530
  E  E  I  L  T  H  C  Q  T  T  L  K  Y  A  I  K  T  G  H  P
```

Figure 2A

```
TGGAGGAAATTTTGACGCACTGCCAAACAACTCTAAAATATGCGATTAAAACAGGGCATC
      550                 570                 590
  R   Y   F   N   Q   L   S   T   G   L   D   M   V   G   L   A   A   D   W   L
CCCGATATTTTAATCAGCTGTCTACCGGATTGGATATGGTTGGATTAGCAGCAGATTGGT
      610                 630                 650
  T   S   T   A   N   T   N   M   F   T   Y   E   I   A   P   V   F   V   L   L
TGACATCAACAGCAAACACGAACATGTTTACCTATGAGATCGCCCCTGTATTTGTACTAC
      670                 690                 710
  E   Y   V   T   L   K   K   M   R   E   I   I   G   W   P   G   G   S   G   D
TGGAATATGTGACACTAAAGAAAATGAGGGAAATCATTGGCTGGCCAGGAGGCTCTGGCG
      730                 750                 770
  G   I   F   S   P   G   G   A   I   S   N   M   Y   A   M   L   I   A   R   Y
ATGGAATCTTTTCTCCTGGTGGTGCCATCTCCAACATGTACGCCATGCTCATTGCCCGCT
      790                 810                 830
  K   M   F   P   E   V   K   E   K   G   M   A   A   V   P   R   L   I   A   F
ATAAGATGTTTCCAGAAGTCAAGGAAAAGGGGATGGCGGCGGTGCCCAGGCTCATCGCAT
      850                 870                 890
  T   S   E   H   S   H   F   S   L   K   K   G   A   A   A   L   G   I   G   T
TCACGTCAGAGCATAGTCACTTTTCTCTCAAGAAGGGAGCTGCAGCCTTGGGGATCGGAA
      910                 930                 950
  D   S   V   I   L   I   K   C   D   E   R   G   K   M   I   P   S   D   L   E
CAGACAGCGTGATTCTGATTAAATGTGATGAGAGAGGGAAAATGATCCCATCTGACCTTG
      970                 990                1010
  R   R   I   L   E   V   K   Q   K   G   F   V   P   F   L   V   S   A   T   A
AAAGAAGAATCCTTGAAGTCAAACAGAAAGGATTTGTTCCTTTCCTGGTGAGTGCCACAG
     1030                1050                1070
  G   T   T   V   Y   G   A   F   D   P   L   L   A   V   A   D   I   C   K   K
```

Figure 2B

```
CTGGAACCACTGTGTACGGGGCTTTTGATCCTCTCTTGGCTGTAGCTGACATCTGCAAAA
     1090                1110                1130
  Y  K  I  W  M  H  V  D  A  A  W  G  G  G  L  L  M  S  R  K
AATATAAGATCTGGATGCATGTGGATGCTGCTTGGGGTGGAGGGTTACTGATGTCTCGGA
     1150                1170                1190
  H  K  W  K  L  N  G  V  E  R  A  N  S  V  T  W  N  P  H  K
AACACAAGTGGAAGCTGAACGGTGTGGAGAGGGCCAACTCTGTGACATGGAATCCCCACA
     1210                1230                1250
  M  M  G  V  P  L  Q  C  S  A  L  L  V  R  E  E  G  L  M  Q
AGATGATGGGTGTCCCCTTGCAATGTTCGGCTCTCCTGGTCAGAGAGGAGGGACTGATGC
     1270                1290                1310
  S  C  N  Q  M  H  A  S  Y  L  F  Q  Q  D  K  H  Y  D  L  S
AGAGCTGCAACCAGATGCATGCTTCCTACCTCTTTCAGCAAGATAAGCACTATGACCTGT
     1330                1350                1370
  Y  D  T  G  D  K  A  L  Q  C  G  R  H  V  D  V  F  K  L  W
CCTATGACACGGGAGACAAGGCCTTGCAGTGTGGACGCCACGTCGATGTCTTTAAATTAT
     1390                1410                1430
  L  M  W  R  A  K  G  T  T  G  F  E  A  H  I  D  K  C  L  E
GGCTCATGTGGAGAGCAAAGGGGACTACTGGATTTGAAGCTCACATTGATAAGTGTTTGG
     1450                1470                1490
  L  A  E  Y  L  Y  N  I  I  K  N  R  E  G  Y  E  M  V  F  D
AGCTGGCAGAGTATTTATACAATATCATTAAAAACCGAGAAGGATATGAAATGGTGTTCG
     1510                1530                1550
  G  K  P  Q  H  T  N  V  C  F  W  F  V  P  P  S  L  R  V  L
ATGGGAAGCCTCAGCACACAAATGTCTGCTTCTGGTTTGTACCTCCTAGTTTGCGAGTTC
     1570                1590                1610
  E  D  N  E  E  R  M  S  R  L  S  K  V  A  P  V  I  K  A  R
```

Figure 2C

```
TGGAAGACAATGAAGAGAGAATGAGCCGCCTCTCAAAGGTGGCGCCAGTGATTAAAGCCA
      1630                 1650                 1670
  M   M   E   Y   G   T   T   M   V   S   Y   Q   P   L   G   D   K   V   N   F
GAATGATGGAGTATGGGACCACAATGGTCAGCTACCAACCCTTAGGAGATAAGGTCAACT
      1690                 1710                 1730
  F   R   M   V   I   S   N   P   A   A   T   H   Q   D   I   D   F   L   I   E
TCTTCCGCATGGTCATCTCAAACCCTGCAGCAACTCACCAAGACATTGACTTCCTCATTG
      1750                 1770                 1790
  E   I   E   R   L   G   Q   D   L   *
AAGAAATCGAACGCCTGGGACAAGATTTGTAATCACTTTGCTCACCAAACTTTCAGTTCT
      1810                 1830                 1850
CTAGGTAGACAGCTAAGTTGTCACAAACTGTGTAAATGTATTTGTAGTTTGTTCCAGAGT
      1870                 1890                 1910
AATTCTATTTCTATATCGTGGTGTCACAGTAGAGTCCAGTTTAAAA
      1930                 1950
```

Figure 2D

```
                                                          M  A  S
AGCTCGCCCGCAGCTCGCACTCGCAGGCGACCTGCTCCAGTCTCCAAAGCCGATGGCATC
        10                  30                  50
 P  G  S  G  F  W  S  F  G  S  E  D  G  S  G  D  S  E  N  P
TCCGGGCTCTGGCTTTTGGTCTTTCGGGTCGGAAGATGGCTCTGGGGATTCCGAGAATCC
        70                  90                  110
 G  T  A  R  A  W  C  Q  V  A  Q  K  F  T  G  G  I  G  N  K
CGGCACAGCGCGAGCCTGGTGCCAAGTGGCTCAGAAGTTCACGGGCGGCATCGGAAACAA
       130                 150                 170
 L  C  A  L  L  Y  G  D  A  E  K  P  A  E  S  G  G  S  Q  P
ACTGTGCGCCCTGCTCTACGGAGACGCCGAGAAGCCGGCGGAGAGCGGCGGGAGCCAACC
       190                 210                 230
 P  R  A  A  A  R  K  A  A  C  A  C  D  Q  K  P  C  S  C  S
CCCGCGGGCCGCCGCCCGGAAGGCCGCCTGCGCCTGCGACCAGAAGCCCTGCAGCTGCTC
       250                 270                 290
 K  V  D  V  N  Y  A  F  L  H  A  T  D  L  L  P  A  C  D  G
CAAAGTGGATGTCAACTACGCGTTTCTCCATGCAACAGACCTGCTGCCGGCGTGTGATGG
       310                 330                 350
 E  R  P  T  L  A  F  L  Q  D  V  M  N  I  L  L  Q  Y  V  V
AGAAAGGCCCACTTTGGCGTTTCTGCAAGATGTTATGAACATTTTACTTCAGTATGTGGT
       370                 390                 410
 K  S  F  D  R  S  T  K  V  I  D  F  H  Y  P  N  E  L  L  Q
GAAAAGTTTCGATAGATCAACCAAAGTGATTGATTTCCATTATCCTAATGAGCTTCTCCA
       430                 450                 470
 E  Y  N  W  E  L  A  D  Q  P  Q  N  L  E  E  I  L  M  H  C
AGAATATAATTGGGAATTGGCAGACCAACCACAAAATTTGGAGGAAATTTTGATGCATTG
```

Figure 3A

```
      490                 510                 530
 Q  T  T  L  K  Y  A  I  K  T  G  H  P  R  Y  F  N  Q  L  S
CCAAACAACTCTAAAATATGCAATTAAAACAGGGCATCCTAGATACTTCAATCAACTTTC
      550                 570                 590
 T  G  L  D  M  V  G  L  A  A  D  W  L  T  S  T  A  N  T  N
TACTGGTTTGGATATGGTTGGATTAGCAGCAGACTGGCTGACATCAACAGCAAATACTAA
      610                 630                 650
 M  F  T  Y  E  I  A  P  V  F  V  L  L  E  Y  V  T  L  K  K
CATGTTCACCTATGAAATTGCTCCAGTATTTGTGCTTTTGGAATATGTCACACTAAAGAA
      670                 690                 710
 M  R  E  I  I  G  W  P  G  G  S  G  D  G  I  F  S  P  G  G
AATGAGAGAAATCATTGGCTGGCCAGGGGGCTCTGGCGATGGGATATTTTCTCCCGGTGG
      730                 750                 770
 A  I  S  N  M  Y  A  M  M  I  A  R  F  K  M  F  P  E  V  K
CGCCATATCTAACATGTATGCCATGATGATCGCACGCTTTAAGATGTTCCCAGAAGTCAA
      790                 810                 830
 E  K  G  M  A  A  L  P  R  L  I  A  F  T  S  E  H  S  H  F
GGAGAAAGGAATGGCTGCTCTTCCCAGGCTCATTGCCTTCACGTCTGAACATAGTCATTT
      850                 870                 890
 S  L  K  K  G  A  A  A  L  G  I  G  T  D  S  V  I  L  I  K
TTCTCTCAAGAAGGGAGCTGCAGCCTTAGGGATTGGAACAGACAGCGTGATTCTGATTAA
      910                 930                 950
 C  D  E  R  G  K  M  I  P  S  D  L  E  R  R  I  L  E  A  K
ATGTGATGAGAGAGGGAAAATGATTCCATCTGATCTTGAAAGAAGGATTCTTGAAGCCAA
      970                 990                1010
 Q  K  G  F  V  P  F  L  V  S  A  T  A  G  T  T  V  Y  G  A
```

Figure 3B

```
ACAGAAAGGGTTTGTTCCTTTCCTCGTGAGTGCCACAGCTGGAACCACCGTGTACGGAGC
      1030                1050                1070
 F  D  P  L  L  A  V  A  D  I  C  K  K  Y  K  I  W  M  H  V
ATTTGACCCCCTCTTAGCTGTCGCTGACATTTGCAAAAAGTATAAGATCTGGATGCATGT
      1090                1110                1130
 D  A  A  W  G  G  G  L  L  M  S  R  K  H  K  W  K  L  S  G
GGATGCAGCTTGGGGTGGGGGATTACTGATGTCCCGAAAACACAAGTGGAAACTGAGTGG
      1150                1170                1190
 V  E  R  A  N  S  V  T  W  N  P  H  K  M  M  G  V  P  L  Q
CGTGGAGAGGGCCAACTCTGTGACGTGGAATCCACACAAGATGATGGGAGTCCCTTTGCA
      1210                1230                1250
 C  S  A  L  L  V  R  E  E  G  L  M  Q  N  C  N  Q  M  H  A
GTGCTCTGCTCTCCTGGTTAGAGAAGAGGGATTGATGCAGAATTGCAACCAAATGCATGC
      1270                1290                1310
 S  Y  L  F  Q  Q  D  K  H  Y  D  L  S  Y  D  T  G  D  K  A
CTCCTACCTCTTTCAGCAAGATAAACATTATGACCTGTCCTATGACACTGGAGACAAGGC
      1330                1350                1370
 L  Q  C  G  R  H  V  D  V  F  K  L  W  L  M  W  R  A  K  G
CTTACAGTGCGGACGCCACGTTGATGTTTTTAAACTATGGCTGATGTGGAGGGCAAAGGG
      1390                1410                1430
 T  T  G  F  E  A  H  V  D  K  C  L  E  L  A  E  Y  L  Y  N
GACTACCGGGTTTGAAGCGCATGTTGATAAATGTTTGGAGTTGGCAGAGTATTTATACAA
      1450                1470                1490
 I  I  K  N  R  E  G  Y  E  M  V  F  D  G  K  P  Q  H  T  N
CATCATAAAAAACCGAGAAGGATATGAGATGGTGTTTGATGGGAAGCCTCAGCACACAAA
      1510                1530                1550
```

Figure 3C

```
 V  C  F  W  Y  I  P  P  S  L  R  T  L  E  D  N  E  E  R  M
TGTCTGCTTCTGGTACATTCCTCCAAGCTTGCGTACTCTGGAAGACAATGAAGAGAGAAT
      1570                 1590                 1610
 S  R  L  S  K  V  A  P  V  I  K  A  R  M  M  E  Y  G  T  T
GAGTCGCCTCTCGAAGGTGGCTCCAGTGATTAAAGCCAGAATGATGGAGTATGGAACCAC
      1630                 1650                 1670
 M  V  S  Y  Q  P  L  G  D  K  V  N  F  F  R  M  V  I  S  N
AATGGTCAGCTACCAACCCTTGGGAGACAAGGTCAATTTCTTCCGCATGGTCATCTCAAA
      1690                 1710                 1730
 P  A  A  T  H  Q  D  I  D  F  L  I  E  E  I  E  R  L  G  Q
CCCAGCGGCAACTCACCAAGACATTGACTTCCTGATTGAAGAAATAGAACGCCTTGGACA
      1750                 1770                 1790
 D  L  *
AGATTTATAATAACCTTGCTCACCAAGCTGTTCCACTTCTCTAGGTAGACAATTAAGTTG
      1810                 1830                 1850
TCACAAACTGTGTGAATGTATTTGTAGTTTGTTCCAAAGTAAATCTATTTCTATATTGTG
      1870                 1890                 1910
GTGTCAAAGTAGAGTTTAAAAATTAAACAAAAAAGACATTGCTCCTTTTAAAAGTCCTTT
      1930                 1950                 1970
CTTAAGTTTAGAATACCTCTCTAAGAATTCGTGACAAAAGGCTATGTTCTAATCAATAAG
      1990                 2010                 2030
GAAAAGCTTAAAATTGTTATAAATACTTCCCTTACTTTTAATATAGTGTGCAAAGCAAAC
      2050                 2070                 2090
```

Figure 3D

GAP WEIGHT: 3.000 LENGTH WEIGHT: 0.100 QUALITY: 856.2 RATIO: 1.464
PERCENT SIMILARITY: 97.436 4817, PEP HGT2.PEP AVERAGE MATCH: 0.540
AVERAGE MISMATCH: -0.396 LENGTH: 585 GAPS: 0 PERCENT IDENTITY: 96.068
AUGUST 22, 1990 08:20 **

```
                .         .         .         .         .
  1 MASPGSGFWSFGSEDGSGDPENPGTARAWCQVAQKFTGGIGNKLCALLYG 50
    |||||||||||||||||||.|||||||||||||||||||||||||||||
  1 MASPGSGFWSFGSEDGSGDSENPGTARAWCQVAQKFTGGIGNKLCALLYG 50
                .         .         .         .         .
 51 DSEKPAESGGSVTSRAATRKVACTCDQKPCSCPKGDVNYALLHATDLLPA 100
    |.|||||||||  ..|||.||.||.||||||||.|.|||||:|||||||||
 51 DAEKPAESGGSQPPRAAARKAACACDQKPCSCSKVDVNYAFLHATDLLPA 100
                .         .         .         .         .
101 CEGERPTLAFLQDVMNILLQYVVKSFDRSTKVIDFHYPNELLQEYNWELA 150
    |:||||||||||||||||||||||||||||||||||||||||||||||||
101 CDGERPTLAFLQDVMNILLQYVVKSFDRSTKVIDFHYPNELLQEYNWELA 150
                .         .         .         .         .
151 DQPQNLEEILTHCQTTLKYAIKTGHPRYFNQLSTGLDMVGLAADWLTSTA 200
    |||||||||| ||||||||||||||||||||||||||||||||||||||||
151 DQPQNLEEILMHCQTTLKYAIKTGHPRYFNQLSTGLDMVGLAADWLTSTA 200
                .         .         .         .         .
201 NTNMFTYEIAPVFVLLEYVTLKKMREIIGWPGGSGDGIFSPGGAISNMYA 250
    ||||||||||||||||||||||||||||||||||||||||||||||||||
201 NTNMFTYEIAPVFVLLEYVTLKKMREIIGWPGGSGDGIFSPGGAISNMYA 250
```

Figure 4A

```
251 MLIARYKMFPEVKEKGMAAVPRLIAFTSEHSHFSLKKGAAALGIGTDSVI 300
    |:|||:|||||||||||||:|||||||||||||||||||||||||||||||
251 MMIARFKMFPEVKEKGMAALPRLIAFTSEHSHFSLKKGAAALGIGTDSVI 300

301 LIKCDERGKMIPSDLERRILEVKQKGFVPFLVSATAGTTVYGAFDPLLAV 350
    |||||||||||||||||||.|||||||||||||||||||||||||||||
301 LIKCDERGKMIPSDLERRILEAKQKGFVPFLVSATAGTTVYGAFDPLLAV 350

351 ADICKKYKIWMHVDAAWGGGLLMSRKHKWKLNGVERANSVTWNPHKMMGV 400
    |||||||||||||||||||||||||||||.||||||||||||||||||||
351 ADICKKYKIWMHVDAAWGGGLLMSRKHKWKLSGVERANSVTWNPHKMMGV 400

401 PLQCSALLVREEGLMQSCNQMHASYLFQQDKHYDLSYDTGDKALQCGRHV 450
    |||||||||||||||.|||||||||||||||||||||||||||||||||
401 PLQCSALLVREEGLMQNCNQMHASYLFQQDKHYDLSYDTGDKALQCGRHV 450

451 DVFKLWLMWRAKGTTGFEAHIDKCLELAEYLYNIIKNREGYEMVFDGKPQ 500
    |||||||||||||||||||:|||||||||||||||||||||||||||||
451 DVFKLWLMWRAKGTTGFEAHVDKCLELAEYLYNIIKNREGYEMVFDGKPQ 500

501 HTNVCFWFVPPSLRVLEDNEERMSRLSKVAPVIKARMMEYGTTMVSYQPL 550
    |||||||::|||||.|||||||||||||||||||||||||||||||||||
501 HTNVCFWYIPPSLRTLEDNEERMSRLSKVAPVIKARMMEYGTTMVSYQPL 550

551 GDKVNFFRMVISNPAATHQDIDFLIEEIERLGQDL 585
    |||||||||||||||||||||||||||||||||||
551 GDKVNFFRMVISNPAATHQDIDFLIEEIERLGQDL 585
```

Figure 4B

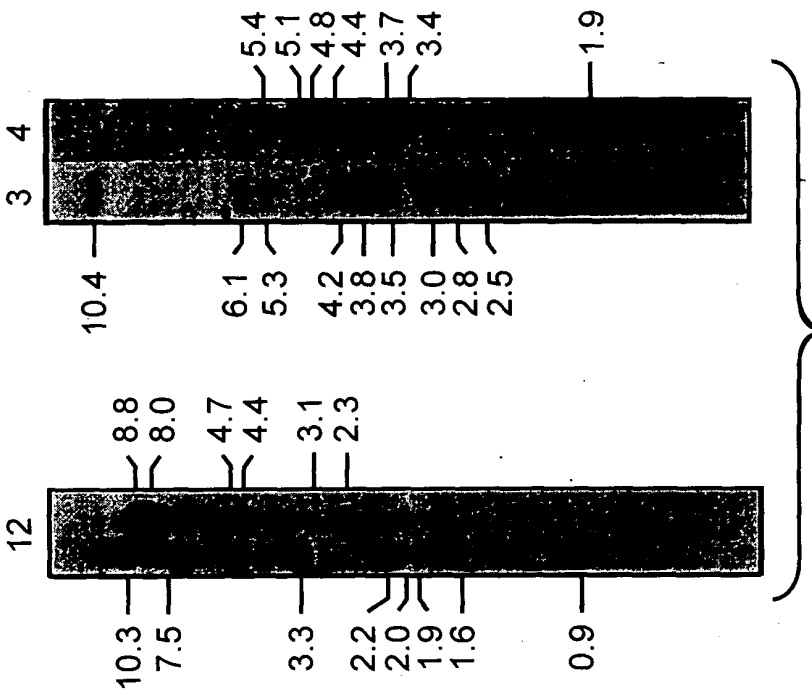

Figure 6

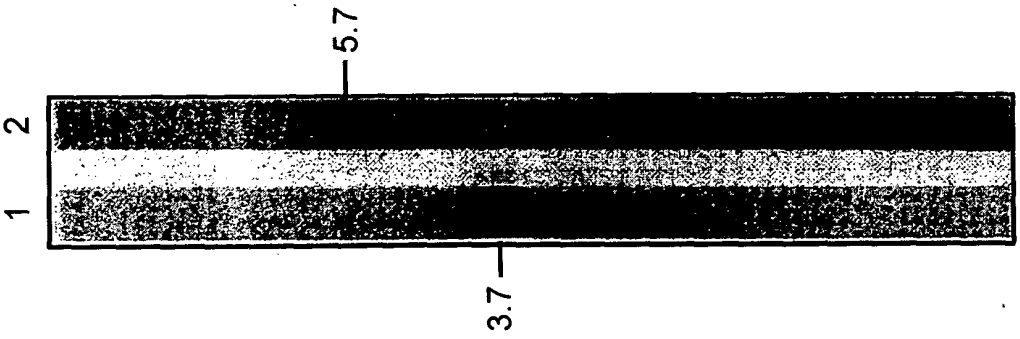

Figure 5

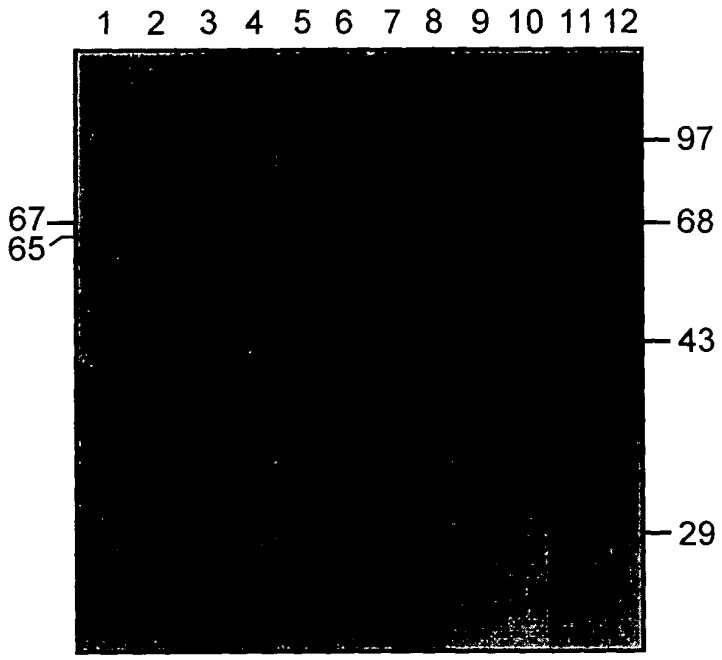

Figure 7